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FILE REFERENCE: PI-0070 USN
CURRENT APPLICATION NUMBER: US/10/258, 080
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 60/203,509
PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: US 60/202,234
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/200,185
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/198,403
PRIOR FILING DATE: 2000-04-19
PRIOR APPLICATION NUMBER: PCT/US01/11869
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: US 60/197,590
PRIOR FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PERL Program
SEQ ID NO 16
LENGTH: 2620
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040029125A1 1272843CB1
US-10-258-080-16

Alignment Scores:
Pred. No.:
Score: 5.87e-314
Percent Similarity: 2615.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 13 Gaps: 0

US-10-669-693-2 (1-504) x US-10-258-080-16 (1-2620)
QY 1 MetGValaIaThrGlyThrTPalaleuLeuLeuIaIaLeuLeuLeuLeuThr 20
Db 41 ATGAGGACACCGGACCTGCGGCGCTGCTGCGCGCTGCTGCTGCTGCTGACG 100
QY 21 LeuAlaLeuSerGlyIhThrTgAlaIaTgGlyVhIstLeuProProGlyProThrProLeuPro 40
Db 101 CTGGCGCTGTCCGGAGCCAGGGGCGGAGGCCACTCTCCCCCGGGGCCACGGCGCTACCA 160
QY 41 LeuLeuGlyAsnLeuLeuGlnLeuAlaTgProGlyAlaLeuTySerGlyLeuMetAlaGLeu 60

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QY	61	SettysLysETyrGlyProValPheThrIleTyrLeuGlyProThrArgProValIVal	80
Db	221	AGTAAMAATACGGACCGGTGTTCACCACTACCTGGACCCCTGGCGGCTGTGGTGTC	280
QY	81	LeuValGIgIingIuValaValaArgIuaIaLeuGIgIyGInaIaGluGInaIuGInuPheSerGIy	100
Db	281	CTGGTTGGGCAAGGAGGCTGTGGCGGAGGGCCCTGGGAGGTCAAGCTAGAGATTCAAGGCGC	340
QY	101	ArgGIyThValAlaMetLeuGluGIyThrPheAspGIyHISGIyValPhePheSerAsn	120
Db	341	CGGGGACCGTIGCCGATGCTGGAAAGGACATTTTGAAGGCCCATGGGCTTTCTCTCCAC	400
QY	121	GIyGIyArgTyrArgGInaLeuArgIyPheThrMetLeuAlaLeuArgAspLeuGIyMet	140
Db	401	GGGGAGCGGTGGAGGAGAGCTGAAGAAATTACATGCTTGCTTGGCGGACCTGGGATG	460
QY	141	GIyLysArgGIuGIyGluGluLeuIleGInaIaGInaIaArgCysLeuValGIuThrPhe	160
Db	461	GGGAAGCGAAGAGGCGACGATGATCCAGCGGAGCCCGGTGTGTGGTGGAGACATTC	520
QY	161	GIyGIyThGIuGIyAArgProPheAspProSerLeuLeuLeuAlaGInaIaThrSerAsn	180
Db	521	CAGGGACAGAAAGGAGCGCCATTGCATCCCTCCCTGCTGAGCCAGGCCACCTCCAC	580
QY	181	ValIValCysSerLeuLeuPheGlyLeuArgPheSerTyrGIuAspIyGluPheGInaIa	200

